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SEQUENCE LISTING

<110> AGO, HIDEO
MIYANO, MASASHI
ADACHI, TSUYOSHI

<120> HCV POLYMERASE SUITABLE FOR CRYSTAL STRUCTURE ANALYSIS
AND METHOD FOR USING THE ENZYME

<130> 09299.0002-00000

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<141> 2000-06-30

<150> JP 11-188630

<151> 1999-07-02

<150> JP 11-192488

<151> 1999-07-07

<160> 28

<170> PatentIn Ver. 2.1

<210> 1

<211> 591

<212> PRT

<213> Hepatitis C virus

<400> 1

Ser Met Ser Tyr Thr Trp Thr Gly Ala Leu Ile Thr Pro Cys Ala Ala
1 5 10 15

Glu Glu Ser Lys Leu Pro Ile Asn Ala Leu Ser Asn Ser Leu Leu Arg
20 25 30

His His Asn Met Val Tyr Ala Thr Thr Ser Arg Ser Ala Gly Leu Arg
35 40 45

Gln Lys Lys Val Thr Phe Asp Arg Leu Gln Val Leu Asp Asp His Tyr
50 55 60

Arg Asp Val Leu Lys Glu Met Lys Ala Lys Ala Ser Thr Val Lys Ala
65 70 75 80

Lys Leu Leu Ser Val Glu Glu Ala Cys Lys Leu Thr Pro Pro His Ser
85 90 95

Ala Lys Ser Lys Phe Gly Tyr Gly Ala Lys Asp Val Arg Asn Leu Ser
100 105 110

Ser Lys Ala Val Asn His Ile His Ser Val Trp Lys Asp Leu Leu Glu
115 120 125

Asp	Thr	Val	Thr	Pro	Ile	Asp	Thr	Thr	Ile	Met	Ala	Lys	Asn	Glu	Val	130	135	140
Phe	Cys	Val	Gln	Pro	Glu	Lys	Gly	Gly	Arg	Lys	Pro	Ala	Arg	Leu	Ile	145	150	155
Val	Phe	Pro	Asp	Leu	Gly	Val	Arg	Val	Cys	Glu	Lys	Met	Ala	Leu	Tyr	165	170	175
Asp	Val	Val	Ser	Thr	Leu	Pro	Gln	Val	Val	Met	Gly	Ser	Ser	Tyr	Gly	180	185	190
Phe	Gln	Tyr	Ser	Pro	Gly	Gln	Arg	Val	Glu	Phe	Leu	Val	Asn	Thr	Trp	195	200	205
Lys	Ser	Lys	Lys	Asn	Pro	Met	Gly	Phe	Ser	Tyr	Asp	Thr	Arg	Cys	Phe	210	215	220
Asp	Ser	Thr	Val	Thr	Glu	Asn	Asp	Ile	Arg	Val	Glu	Glu	Ser	Ile	Tyr	225	230	235
Gln	Cys	Cys	Asp	Leu	Ala	Pro	Glu	Ala	Arg	Gln	Ala	Ile	Lys	Ser	Leu	245	250	255
Thr	Glu	Arg	Leu	Tyr	Ile	Gly	Gly	Pro	Leu	Thr	Asn	Ser	Lys	Gly	Gln	260	265	270
Asn	Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Leu	Thr	Thr	Ser	275	280	285
Cys	Gly	Asn	Thr	Leu	Thr	Cys	Tyr	Leu	Lys	Ala	Ser	Ala	Ala	Cys	Arg	290	295	300
Ala	Ala	Lys	Leu	Gln	Asp	Cys	Thr	Met	Leu	Val	Asn	Gly	Asp	Asp	Leu	305	310	315
Val	Val	Ile	Cys	Glu	Ser	Ala	Gly	Thr	Gln	Glu	Asp	Ala	Ala	Ser	Leu	325	330	335
Arg	Val	Phe	Thr	Glu	Ala	Met	Thr	Arg	Tyr	Ser	Ala	Pro	Pro	Gly	Asp	340	345	350
Pro	Pro	Gln	Pro	Glu	Tyr	Asp	Leu	Glu	Leu	Ile	Thr	Ser	Cys	Ser	Ser	355	360	365
Asn	Val	Ser	Val	Ala	His	Asp	Ala	Ser	Gly	Lys	Arg	Val	Tyr	Tyr	Leu	370	375	380
Thr	Arg	Asp	Pro	Thr	Thr	Pro	Leu	Ala	Arg	Ala	Ala	Trp	Glu	Thr	Ala	385	390	395
Arg	His	Thr	Pro	Val	Asn	Ser	Trp	Leu	Gly	Asn	Ile	Ile	Met	Tyr	Ala	405	410	415

Pro Thr Leu Trp Ala Arg Met Ile Leu Met Thr His Phe Phe Ser Ile
420 425 430

Leu Leu Ala Gln Glu Gln Leu Glu Lys Ala Leu Asp Cys Gln Ile Tyr
435 440 445

Gly Ala Cys Tyr Ser Ile Glu Pro Leu Asp Leu Pro Gln Ile Ile Glu
450 455 460

Arg Leu His Gly Leu Ser Ala Phe Ser Leu His Ser Tyr Ser Pro Gly
465 470 475 480

Glu Ile Asn Arg Val Ala Ser Cys Leu Arg Lys Leu Gly Val Pro Pro
485 490 495

Leu Arg Val Trp Arg His Arg Ala Arg Ser Val Arg Ala Arg Leu Leu
500 505 510

Ser Gln Gly Gly Arg Ala Ala Thr Cys Gly Lys Tyr Leu Phe Asn Trp
515 520 525

Ala Val Lys Thr Lys Leu Lys Leu Thr Pro Ile Pro Ala Ala Ser Gln
530 535 540

Leu Asp Leu Ser Gly Trp Phe Val Ala Gly Tyr Ser Gly Gly Asp Ile
545 550 555 560

Tyr His Ser Leu Ser Arg Ala Arg Pro Arg Trp Phe Met Leu Cys Leu
565 570 575

Leu Leu Leu Ser Val Gly Val Gly Ile Tyr Leu Leu Pro Asn Arg
580 585 590

<210> 2
<211> 1743
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: DNA encoding
fusion protein consisting of a portion of HCV
polymerase and histidine tag at the C-terminus

<220>
<221> CDS
<222> (1)..(1743)

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Met Ser Met Ser Tyr Thr Trp Thr Gly Ala Leu Ile Thr Pro Cys Ala
1 5 10 15

gcg gag gaa agc aag ctg ccc atc aac gcg ttg agc aac tct ttg ctg	96
Ala Glu Glu Ser Lys Leu Pro Ile Asn Ala Leu Ser Asn Ser Leu Leu	
20 25 30	
cgc cac cat aac atg gtt tat gcc aca aca tct cgc agc gca ggc ctg	144
Arg His His Asn Met Val Tyr Ala Thr Thr Ser Arg Ser Ala Gly Leu	
35 40 45	
cgg cag aag aag gtc acc ttt gac aga ctg caa gtc ctg gac gac cac	192
Arg Gln Lys Lys Val Thr Phe Asp Arg Leu Gln Val Leu Asp Asp His	
50 55 60	
tac cgg gac gtg ctc aag gag atg aag gcg aag gcg tcc aca gtt aag	240
Tyr Arg Asp Val Leu Lys Glu Met Lys Ala Lys Ala Ser Thr Val Lys	
65 70 75 80	
gct aaa ctc cta tcc gta gag gaa gcc tgc aag ctg acg ccc cca cat	288
Ala Lys Leu Leu Ser Val Glu Glu Ala Cys Lys Leu Thr Pro Pro His	
85 90 95	
tcg gcc aaa tcc aag ttt ggc tat ggg gca aag gac gtc cgg aac cta	336
Ser Ala Lys Ser Lys Phe Gly Tyr Gly Ala Lys Asp Val Arg Asn Leu	
100 105 110	
tcc agc aag gcc gtt aac cac atc cac tcc gtg tgg aag gac ttg ctg	384
Ser Ser Lys Ala Val Asn His Ile His Ser Val Trp Lys Asp Leu Leu	
115 120 125	
gaa gac act gtg aca cca att gac acc acc atc atg gca aaa aat gag	432
Glu Asp Thr Val Thr Pro Ile Asp Thr Thr Ile Met Ala Lys Asn Glu	
130 135 140	
gtt ttc tgt gtc caa cca gag aaa gga ggc cgt aag cca gcc cgc ctt	480
Val Phe Cys Val Gln Pro Glu Lys Gly Gly Arg Lys Pro Ala Arg Leu	
145 150 155 160	
atc gta ttc cca gat ctg gga gtc cgt gta tgc gag aag atg gcc ctc	528
Ile Val Phe Pro Asp Leu Gly Val Arg Val Cys Glu Lys Met Ala Leu	
165 170 175	
tat gat gtg gtc tcc acc ctt cct cag gtc gtg atg ggc tcc tca tac	576
Tyr Asp Val Val Ser Thr Leu Pro Gln Val Val Met Gly Ser Ser Tyr	
180 185 190	
gga ttc cag tac tct cct ggg cag cga gtc gag ttc ctg gtg aat acc	624
Gly Phe Gln Tyr Ser Pro Gly Gln Arg Val Glu Phe Leu Val Asn Thr	
195 200 205	
tgg aaa tca aag aaa aac ccc atg ggc ttt tca tat gac act cgc tgt	672
Trp Lys Ser Lys Lys Asn Pro Met Gly Phe Ser Tyr Asp Thr Arg Cys	
210 215 220	

ttc gac tca acg gtc acc gag aac gac atc cgt gtt gag gag tca att	720
Phe Asp Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Glu Ser Ile	
225 230 235 240	
tac caa tgt tgt gac ttg gcc ccc gaa gcc aga cag gcc ata aaa tcg	768
Tyr Gln Cys Cys Asp Leu Ala Pro Glu Ala Arg Gln Ala Ile Lys Ser	
245 250 255	
ctc aca gag cgg ctt tat atc ggg ggt cct ctg act aat tca aaa ggg	816
Leu Thr Glu Arg Leu Tyr Ile Gly Gly Pro Leu Thr Asn Ser Lys Gly	
260 265 270	
cag aac tgc ggt tat cgc cgg tgc cgc gcg agc ggc gtg ctg acg act	864
Gln Asn Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr	
275 280 285	
agc tgc ggt aac acc ctc aca tgt tac ttg aag gcc tct gca gcc tgt	912
Ser Cys Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Cys	
290 295 300	
cga gct gcg aag ctc cag gac tgc acg atg ctc gtg aac gga gac gac	960
Arg Ala Ala Lys Leu Gln Asp Cys Thr Met Leu Val Asn Gly Asp Asp	
305 310 315 320	
ctc gtc gtt atc tgt gaa agc gcg gga acc caa gag gac gcg gcg agc	1008
Leu Val Val Ile Cys Glu Ser Ala Gly Thr Gln Glu Asp Ala Ala Ser	
325 330 335	
cta cga gtc ttc acg gag gct atg act agg tac tcc gcc ccc ccc ggg	1056
Leu Arg Val Phe Thr Glu Ala Met Thr Arg Tyr Ser Ala Pro Pro Gly	
340 345 350	
gac ccg ccc caa cca gaa tac gac ttg gag ctg ata aca tca tgt tcc	1104
Asp Pro Pro Gln Pro Glu Tyr Asp Leu Glu Leu Ile Thr Ser Cys Ser	
355 360 365	
tcc aat gtg tcg gtc gcc cac gat gca tca ggc aaa agg gtg tac tac	1152
Ser Asn Val Ser Val Ala His Asp Ala Ser Gly Lys Arg Val Tyr Tyr	
370 375 380	
ctc acc cgt gat ccc acc acc ccc ctc gca cgg gct gcg tgg gag aca	1200
Leu Thr Arg Asp Pro Thr Thr Pro Leu Ala Arg Ala Ala Trp Glu Thr	
385 390 395 400	
gct aga cac act cca gtt aac tcc tgg cta ggc aac att att atg tat	1248
Ala Arg His Thr Pro Val Asn Ser Trp Leu Gly Asn Ile Ile Met Tyr	
405 410 415	
gcg ccc act ttg tgg gca agg atg att ctg atg act cac ttc ttc tcc	1296
Ala Pro Thr Leu Trp Ala Arg Met Ile Leu Met Thr His Phe Phe Ser	
420 425 430	

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atc ctt cta gcg cag gag caa ctt gaa aaa gcc ctg gac tgc cag atc      1344
Ile Leu Leu Ala Gln Glu Gln Leu Glu Lys Ala Leu Asp Cys Gln Ile
      435                      440                      445

tac ggg gcc tgt tac tcc att gag cca ctt gac cta cct cag atc att      1392
Tyr Gly Ala Cys Tyr Ser Ile Glu Pro Leu Asp Leu Pro Gln Ile Ile
      450                      455                      460

gaa cga ctc cat ggc ctt agc gca ttt tca ctc cat agt tac tct cca      1440
Glu Arg Leu His Gly Leu Ser Ala Phe Ser Leu His Ser Tyr Ser Pro
465                      470                      475                      480

ggt gag atc aat agg gtg gct tca tgc ctc agg aaa ctt ggg gta cca      1488
Gly Glu Ile Asn Arg Val Ala Ser Cys Leu Arg Lys Leu Gly Val Pro
      485                      490                      495

ccc ttg cga gtc tgg aga cat cgg gcc agg agc gtc cgc gct agg cta      1536
Pro Leu Arg Val Trp Arg His Arg Ala Arg Ser Val Arg Ala Arg Leu
      500                      505                      510

ctg tcc cag ggg ggg agg gcc gcc act tgt ggc aag tac ctc ttc aac      1584
Leu Ser Gln Gly Gly Arg Ala Ala Thr Cys Gly Lys Tyr Leu Phe Asn
      515                      520                      525

tgg gca gtg aag acc aaa ctc aaa ctc act cca atc ccg gct gcg tcc      1632
Trp Ala Val Lys Thr Lys Leu Lys Leu Thr Pro Ile Pro Ala Ala Ser
      530                      535                      540

cag ctg gac ttg tcc ggc tgg ttc gtt gct ggt tac agc ggg gga gac      1680
Gln Leu Asp Leu Ser Gly Trp Phe Val Ala Gly Tyr Ser Gly Gly Asp
545                      550                      555                      560

ata tat cac agc ctg tct cgt gcc cga ccc cgc gga tcc cat cac cat      1728
Ile Tyr His Ser Leu Ser Arg Ala Arg Pro Arg Gly Ser His His His
      565                      570                      575

cac cat cac taa taa
His His His
      1743

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<210> 3
<211> 579
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Fusion protein
      consisting of a portion of HCV polymerase and
      histidine tag at the C-terminus

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<400> 3
Met Ser Met Ser Tyr Thr Trp Thr Gly Ala Leu Ile Thr Pro Cys Ala
  1              5              10              15

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Ala Glu Glu Ser Lys Leu Pro Ile Asn Ala Leu Ser Asn Ser Leu Leu
 20 25 30

Arg His His Asn Met Val Tyr Ala Thr Thr Ser Arg Ser Ala Gly Leu
 35 40 45

Arg Gln Lys Lys Val Thr Phe Asp Arg Leu Gln Val Leu Asp Asp His
 50 55 60

Tyr Arg Asp Val Leu Lys Glu Met Lys Ala Lys Ala Ser Thr Val Lys
 65 70 75 80

Ala Lys Leu Leu Ser Val Glu Glu Ala Cys Lys Leu Thr Pro Pro His
 85 90 95

Ser Ala Lys Ser Lys Phe Gly Tyr Gly Ala Lys Asp Val Arg Asn Leu
 100 105 110

Ser Ser Lys Ala Val Asn His Ile His Ser Val Trp Lys Asp Leu Leu
 115 120 125

Glu Asp Thr Val Thr Pro Ile Asp Thr Thr Ile Met Ala Lys Asn Glu
 130 135 140

Val Phe Cys Val Gln Pro Glu Lys Gly Gly Arg Lys Pro Ala Arg Leu
 145 150 155 160

Ile Val Phe Pro Asp Leu Gly Val Arg Val Cys Glu Lys Met Ala Leu
 165 170 175

Tyr Asp Val Val Ser Thr Leu Pro Gln Val Val Met Gly Ser Ser Tyr
 180 185 190

Gly Phe Gln Tyr Ser Pro Gly Gln Arg Val Glu Phe Leu Val Asn Thr
 195 200 205

Trp Lys Ser Lys Lys Asn Pro Met Gly Phe Ser Tyr Asp Thr Arg Cys
 210 215 220

Phe Asp Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Glu Ser Ile
 225 230 235 240

Tyr Gln Cys Cys Asp Leu Ala Pro Glu Ala Arg Gln Ala Ile Lys Ser
 245 250 255

Leu Thr Glu Arg Leu Tyr Ile Gly Gly Pro Leu Thr Asn Ser Lys Gly
 260 265 270

Gln Asn Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr
 275 280 285

Ser Cys Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Cys
 290 295 300

Arg Ala Ala Lys Leu Gln Asp Cys Thr Met Leu Val Asn Gly Asp Asp
 305 310 315 320
 Leu Val Val Ile Cys Glu Ser Ala Gly Thr Gln Glu Asp Ala Ala Ser
 325 330 335
 Leu Arg Val Phe Thr Glu Ala Met Thr Arg Tyr Ser Ala Pro Pro Gly
 340 345 350
 Asp Pro Pro Gln Pro Glu Tyr Asp Leu Glu Leu Ile Thr Ser Cys Ser
 355 360 365
 Ser Asn Val Ser Val Ala His Asp Ala Ser Gly Lys Arg Val Tyr Tyr
 370 375 380
 Leu Thr Arg Asp Pro Thr Thr Pro Leu Ala Arg Ala Ala Trp Glu Thr
 385 390 395 400
 Ala Arg His Thr Pro Val Asn Ser Trp Leu Gly Asn Ile Ile Met Tyr
 405 410 415
 Ala Pro Thr Leu Trp Ala Arg Met Ile Leu Met Thr His Phe Phe Ser
 420 425 430
 Ile Leu Leu Ala Gln Glu Gln Leu Glu Lys Ala Leu Asp Cys Gln Ile
 435 440 445
 Tyr Gly Ala Cys Tyr Ser Ile Glu Pro Leu Asp Leu Pro Gln Ile Ile
 450 455 460
 Glu Arg Leu His Gly Leu Ser Ala Phe Ser Leu His Ser Tyr Ser Pro
 465 470 475 480
 Gly Glu Ile Asn Arg Val Ala Ser Cys Leu Arg Lys Leu Gly Val Pro
 485 490 495
 Pro Leu Arg Val Trp Arg His Arg Ala Arg Ser Val Arg Ala Arg Leu
 500 505 510
 Leu Ser Gln Gly Gly Arg Ala Ala Thr Cys Gly Lys Tyr Leu Phe Asn
 515 520 525
 Trp Ala Val Lys Thr Lys Leu Lys Leu Thr Pro Ile Pro Ala Ala Ser
 530 535 540
 Gln Leu Asp Leu Ser Gly Trp Phe Val Ala Gly Tyr Ser Gly Gly Asp
 545 550 555 560
 Ile Tyr His Ser Leu Ser Arg Ala Arg Pro Arg Gly Ser His His His
 565 570 575
 His His His

<210> 4
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer, 5BNdelFW

<220>
 <221> primer_bind
 <222> (1)..(30)

<400> 4
 catatgtcaa tgcctacac atggacagcc

30

<210> 5
 <211> 57
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer, 5B570HRV

<220>
 <221> primer_bind
 <222> (1)..(57)

<400> 5
 ttattagtga tggatgatggt gatgggatcc gcgggggctcgg gcacgagaca ggctgtg

57

<210> 6
 <211> 57
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer, 5B552HRV

<220>
 <221> primer_bind
 <222> (1)..(57)

<400> 6
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57

<210> 7
 <211> 57
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer, 5B544HRV

<220>
 <221> primer_bind
 <222> (1)..(57)

<400> 7
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<210> 8
 <211> 67
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer, 5B536HRV

<220>
 <221> primer_bind
 <222> (1)..(67)

<400> 8
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 gaagagg 67

<210> 9
 <211> 60
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer, 5B531HRV

<220>
 <221> primer_bind
 <222> (1)..(60)

<400> 9
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<210> 10
 <211> 52
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer, 5B591HRV

<220>
 <221> primer_bind
 <222> (1)..(52)

<400> 10
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52

<210> 11
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 <212> PRT
 <213> Hepatitis C virus

<220>
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 <222> (1)..(3)
 <223> Variable amino acid or not present

<220>
 <221> MOD_RES
 <222> (5)..(6)
 <223> Variable amino acid

<220>
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 <222> (9)
 <223> Variable amino acid or not present

<400> 11
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<210> 12
 <211> 8
 <212> PRT
 <213> Hepatitis C virus

<400> 12
 Lys Asp Leu Ser Gly Trp Phe Lys
 1 5

<210> 13
<211> 9
<212> PRT
<213> Hepatitis C virus

<400> 13
Lys Lys Asp Leu Ser Gly Trp Phe Lys
1 5

<210> 14
<211> 8
<212> PRT
<213> Hepatitis C virus

<400> 14
Lys Asp Leu Ser Gly Trp Phe Val
1 5

<210> 15
<211> 8
<212> PRT
<213> Hepatitis C virus

<400> 15
Leu Asp Leu Ser Gly Trp Phe Lys
1 5

<210> 16
<211> 8
<212> PRT
<213> Hepatitis C virus

<400> 16
Leu Asp Leu Ser Gly Trp Phe Val
1 5

<210> 17
<211> 7
<212> PRT
<213> Hepatitis C virus

<400> 17
Asp Leu Ser Gly Trp Phe Val
1 5

<210> 18
<211> 6
<212> PRT
<213> Hepatitis C virus

<400> 18
 Asp Leu Ser Gly Trp Phe
 1 5

<210> 19
 <211> 6
 <212> PRT
 <213> Hepatitis C virus

<400> 19
 Leu Ser Gly Trp Phe Val
 1 5

<210> 20
 <211> 5
 <212> PRT
 <213> Hepatitis C virus

<400> 20
 Leu Ser Gly Trp Phe
 1 5

<210> 21
 <211> 6
 <212> PRT
 <213> Hepatitis C virus

<400> 21
 Leu Ser Gly Trp Phe Lys
 1 5

<210> 22
 <211> 6
 <212> PRT
 <213> Hepatitis C virus

<400> 22
 Lys Leu Ser Gly Trp Phe
 1 5

<210> 23
 <211> 5
 <212> PRT
 <213> Hepatitis C virus

<400> 23
 Leu Gly Gly Trp Phe
 1 5

<210> 24
 <211> 5
 <212> PRT
 <213> Hepatitis C virus

<400> 24
 Leu Ser Asp Trp Phe
 1 5

<210> 25
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 25
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 1 5

<210> 26
 <211> 578
 <212> PRT
 <213> Hepatitis C virus

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Glu Glu Ser Lys Leu Pro Ile Asn Ala Leu Ser Asn Ser Leu Leu Arg
 20 25 30

His His Asn Met Val Tyr Ala Thr Thr Ser Arg Ser Ala Gly Leu Arg
 35 40 45

Gln Lys Lys Val Thr Phe Asp Arg Leu Gln Val Leu Asp Asp His Tyr
 50 55 60

Arg Asp Val Leu Lys Glu Met Lys Ala Lys Ala Ser Thr Val Lys Ala
 65 70 75 80

Lys Leu Leu Ser Val Glu Glu Ala Cys Lys Leu Thr Pro Pro His Ser
 85 90 95

Ala Lys Ser Lys Phe Gly Tyr Gly Ala Lys Asp Val Arg Asn Leu Ser
 100 105 110

Ser Lys Ala Val Asn His Ile His Ser Val Trp Lys Asp Leu Leu Glu
 115 120 125
 Asp Thr Val Thr Pro Ile Asp Thr Thr Ile Met Ala Lys Asn Glu Val
 130 135 140
 Phe Cys Val Gln Pro Glu Lys Gly Gly Arg Lys Pro Ala Arg Leu Ile
 145 150 155 160
 Val Phe Pro Asp Leu Gly Val Arg Val Cys Glu Lys Met Ala Leu Tyr
 165 170 175
 Asp Val Val Ser Thr Leu Pro Gln Val Val Met Gly Ser Ser Tyr Gly
 180 185 190
 Phe Gln Tyr Ser Pro Gly Gln Arg Val Glu Phe Leu Val Asn Thr Trp
 195 200 205
 Lys Ser Lys Lys Asn Pro Met Gly Phe Ser Tyr Asp Thr Arg Cys Phe
 210 215 220
 Asp Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Glu Ser Ile Tyr
 225 230 235 240
 Gln Cys Cys Asp Leu Ala Pro Glu Ala Arg Gln Ala Ile Lys Ser Leu
 245 250 255
 Thr Glu Arg Leu Tyr Ile Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln
 260 265 270
 Asn Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser
 275 280 285
 Cys Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Cys Arg
 290 295 300
 Ala Ala Lys Leu Gln Asp Cys Thr Met Leu Val Asn Gly Asp Asp Leu
 305 310 315 320
 Val Val Ile Cys Glu Ser Ala Gly Thr Gln Glu Asp Ala Ala Ser Leu
 325 330 335
 Arg Val Phe Thr Glu Ala Met Thr Arg Tyr Ser Ala Pro Pro Gly Asp
 340 345 350
 Pro Pro Gln Pro Glu Tyr Asp Leu Glu Leu Ile Thr Ser Cys Ser Ser
 355 360 365
 Asn Val Ser Val Ala His Asp Ala Ser Gly Lys Arg Val Tyr Tyr Lys
 370 375 380
 Thr Arg Asp Pro Thr Thr Pro Leu Ala Arg Ala Ala Trp Glu Thr Ala
 385 390 395 400

Arg His Thr Pro Val Asn Ser Trp Leu Gly Asn Ile Ile Met Tyr Ala
 405 410 415
 Pro Thr Leu Trp Ala Arg Met Ile Leu Met Thr His Phe Phe Ser Ile
 420 425 430
 Leu Leu Ala Gln Glu Gln Leu Glu Lys Ala Leu Asp Cys Gln Ile Tyr
 435 440 445
 Gly Ala Cys Tyr Ser Ile Glu Pro Leu Asp Leu Pro Gln Ile Ile Glu
 450 455 460
 Arg Leu His Gly Leu Ser Ala Phe Ser Leu His Ser Tyr Ser Pro Gly
 465 470 475 480
 Glu Ile Asn Arg Val Ala Ser Cys Leu Arg Lys Leu Gly Val Pro Pro
 485 490 495
 Leu Arg Val Trp Arg His Arg Ala Arg Ser Val Arg Ala Arg Leu Leu
 500 505 510
 Ser Gln Gly Gly Arg Ala Ala Thr Cys Gly Lys Tyr Leu Phe Asn Trp
 515 520 525
 Ala Val Lys Thr Lys Leu Lys Leu Thr Pro Ile Pro Ala Ala Ser Arg
 530 535 540
 Leu Asp Leu Ser Gly Trp Phe Val Ala Gly Tyr Ser Gly Gly Asp Ile
 545 550 555 560
 Tyr His Ser Leu Ser Arg Ala Arg Pro Arg Gly Ser His His His His
 565 570 575
 His His

<210> 27
 <211> 465
 <212> PRT
 <213> Human poliovirus 1

<400> 27
 Met Arg Pro Ser Lys Glu Val Gly Tyr Pro Ile Ile Asn Ala Pro Ser
 1 5 10 15
 Lys Thr Lys Leu Glu Pro Ser Ala Phe His Tyr Val Phe Glu Gly Val
 20 25 30
 Lys Glu Pro Ala Val Leu Thr Lys Asn Asp Pro Arg Leu Lys Thr Asp
 35 40 45
 Phe Glu Glu Ala Ile Phe Ser Lys Tyr Val Gly Asn Lys Ile Thr Glu
 50 55 60

Val	Asp	Glu	Tyr	Met	Lys	Glu	Ala	Val	Asp	His	Tyr	Ala	Gly	Gln	Leu	65	70	75	80
Met	Ser	Leu	Asp	Ile	Asn	Thr	Glu	Gln	Met	Cys	Leu	Glu	Asp	Ala	Met	85	90	95	
Tyr	Gly	Thr	Asp	Gly	Leu	Glu	Ala	Leu	Asp	Leu	Ser	Thr	Ser	Ala	Gly	100	105	110	
Tyr	Pro	Tyr	Val	Ala	Met	Gly	Lys	Lys	Lys	Arg	Asp	Ile	Leu	Asn	Lys	115	120	125	
Gln	Thr	Arg	Asp	Thr	Lys	Glu	Met	Gln	Lys	Leu	Leu	Asp	Thr	Tyr	Gly	130	135	140	
Ile	Asn	Leu	Pro	Leu	Val	Thr	Tyr	Val	Lys	Asp	Glu	Leu	Arg	Ser	Lys	145	150	155	160
Thr	Lys	Val	Glu	Gln	Gly	Lys	Ser	Arg	Leu	Ile	Glu	Ala	Ser	Ser	Gly	165	170	175	
Lys	Ser	Arg	Leu	Ile	Glu	Ala	Ser	Ser	Asn	Asp	Ser	Val	Ala	Met	Arg	180	185	190	
Met	Ala	Phe	Gly	Asn	Leu	Tyr	Ala	Ala	Phe	His	Lys	Asn	Pro	Gly	Val	195	200	205	
Ile	Thr	Gly	Ser	Ala	Val	Gly	Cys	Asp	Pro	Asp	Leu	Phe	Trp	Ser	Lys	210	215	220	
Ile	Pro	Val	Leu	Met	Glu	Glu	Lys	Leu	Phe	Ala	Phe	Asp	Tyr	Thr	Gly	225	230	235	240
Tyr	Asp	Ala	Ser	Leu	Ser	Pro	Ala	Trp	Phe	Glu	Ala	Leu	Lys	Met	Val	245	250	255	
Leu	Glu	Lys	Ile	Gly	Phe	Gly	Asp	Arg	Val	Asp	Tyr	Ile	Asp	Tyr	Leu	260	265	270	
Asn	His	Ser	His	His	Leu	Tyr	Lys	Asn	Lys	Thr	Tyr	Cys	Val	Lys	Gly	275	280	285	
Gly	Met	Pro	Ser	Gly	Cys	Ser	Gly	Thr	Ser	Ile	Phe	Asn	Ser	Met	Ile	290	295	300	
Asn	Asn	Leu	Ile	Ile	Arg	Thr	Leu	Leu	Leu	Lys	Thr	Tyr	Lys	Gly	Ile	305	310	315	320
Asp	Leu	Asp	His	Leu	Lys	Met	Ile	Ala	Tyr	Gly	Asp	Asp	Val	Ile	Ala	325	330	335	
Ser	Tyr	Pro	His	Glu	Val	Asp	Ala	Ser	Leu	Leu	Ala	Gln	Ser	Gly	Lys	340	345	350	

Asp Tyr Gly Leu Thr Met Thr Pro Ala Asp Lys Ser Ala Thr Phe Glu
355 360 365

Thr Val Thr Trp Glu Asn Val Thr Phe Leu Lys Arg Phe Phe Arg Ala
370 375 380

Asp Glu Lys Tyr Pro Phe Leu Ile His Pro Val Met Pro Met Lys Glu
385 390 395 400

Ile His Glu Ser Ile Arg Trp Thr Lys Asp Pro Arg Asn Thr Gln Asp
405 410 415

His Val Arg Ser Leu Cys Leu Leu Ala Trp His Asn Gly Glu Glu Glu
420 425 430

Tyr Asn Lys Phe Leu Ala Lys Ile Arg Ser Val Pro Ile Gly Arg Ala
435 440 445

Leu Leu Leu Pro Glu Tyr Ser Thr Leu Tyr Arg Arg Trp Leu Asp Ser
450 455 460

Phe
465

<210> 28

<211> 320

<212> PRT

<213> Human immunodeficiency virus

<400> 28

Lys Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys Pro Gly Met
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Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu Lys Ile Lys
20 25 30

Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly Lys Ile Ser
35 40 45

Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe Ala Ile Lys
50 55 60

Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg Glu Leu
65 70 75 80

Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile Pro His
85 90 95

Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu Asp Val Gly
100 105 110

Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Glu	Asp	Phe	Arg	Lys	Tyr	Thr	115	120	125
Ala	Phe	Thr	Ile	Pro	Ser	Ile	Asn	Asn	Glu	Thr	Pro	Gly	Ile	Arg	Tyr	130	135	140
Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	Ala	Ile	Phe	145	150	155
Gln	Ser	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys	Gln	Asn	Pro	165	170	175
Asp	Ile	Val	Ile	Tyr	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val	Gly	Ser	Asp	180	185	190
Leu	Glu	Ile	Gly	Gln	His	Arg	Thr	Lys	Ile	Glu	Glu	Leu	Arg	Gln	His	195	200	205
Leu	Leu	Arg	Trp	Gly	Leu	Thr	Thr	Pro	Asp	Lys	Lys	His	Gln	Lys	Glu	210	215	220
Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp	Lys	Trp	Thr	225	230	235
Val	Gln	Pro	Ile	Val	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Thr	Val	Asn	Asp	245	250	255
Ile	Cys	Lys	Leu	Val	Gly	Lys	Leu	Asn	Trp	Ala	Ser	Gln	Ile	Tyr	Pro	260	265	270
Gly	Ile	Lys	Val	Arg	Gln	Leu	Cys	Lys	Leu	Leu	Arg	Gly	Thr	Lys	Ala	275	280	285
Leu	Thr	Glu	Val	Ile	Pro	Leu	Thr	Glu	Glu	Ala	Glu	Leu	Glu	Leu	Ala	290	295	300
Glu	Asn	Arg	Glu	Ile	Leu	Lys	Glu	Pro	Val	His	Gly	Val	Tyr	Tyr	Asp	305	310	315